

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 14

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2261 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 49..1551

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

DDSTT 45/ET/60

CGCAGCACGG	CAACACATAC	ACAGGAGCCA	CACACCGCAC	CTACCCCG	ATG	GAC	GTC	57								
					Met	Asp	Val									
					1											
CTC	CTC	CTG	GAG	AAG	GCC	CTC	CTG	GGC	CTC	TTC	GCC	GCG	GCG	GTG	CTG	105
Leu	Leu	Leu	Glu	Lys	Ala	Leu	Leu	Gly	Leu	Phe	Ala	Ala	Ala	Val	Leu	
		5				10					15					
GCC	ATC	GCC	GTC	GCC	AAG	CTC	ACC	GGC	AAG	CGC	TTC	CGC	CTC	CCC	CCT	153
Ala	Ile	Ala	Val	Ala	Lys	Leu	Thr	Gly	Lys	Arg	Phe	Arg	Leu	Pro	Pro	
20				25					30					35		
GGC	CCC	TCC	GGC	GCC	CCC	ATC	GTC	GGC	AAC	TGG	CTG	CAG	GTC	GGC	GAC	201
Gly	Pro	Ser	Gly	Ala	Pro	Ile	Val	Gly	Asn	Trp	Leu	Gln	Val	Gly	Asp	
			40						45					50		
GAC	CTC	AAC	CAC	CGC	AAC	CTG	ATG	GGC	CTG	GCC	AAG	CGG	TTC	GGC	GAG	249
Asp	Leu	Asn	His	Arg	Asn	Leu	Met	Gly	Leu	Ala	Lys	Arg	Phe	Gly	Glu	
			55					60					65			
GTG	TTC	CTC	CTC	CGC	ATG	GGC	GTC	CGC	AAC	CTG	GTG	GTC	GTC	TCC	AGC	297
Val	Phe	Leu	Leu	Arg	Met	Gly	Val	Arg	Asn	Leu	Val	Val	Val	Ser	Ser	
		70				75						80				
CCC	GAG	CTC	GCC	AAG	GAG	GTC	CTC	CAC	ACC	CAG	GGC	GTC	GAG	TTC	GGC	345
Pro	Glu	Leu	Ala	Lys	Glu	Val	Leu	His	Thr	Gln	Gly	Val	Glu	Phe	Gly	
	85					90					95					
TCC	CGC	ACC	CGC	AAC	GTC	GTC	TTC	GAC	ATC	TTC	ACC	GGC	AAG	GGA	CAG	393
Ser	Arg	Thr	Arg	Asn	Val	Val	Phe	Asp	Ile	Phe	Thr	Gly	Lys	Gly	Gln	
100				105					110					115		
GAC	ATG	GTG	TTC	ACG	GTG	TAC	GGC	GAC	CAC	TGG	CGC	AAG	ATG	CGG	CGG	441
Asp	Met	Val	Phe	Thr	Val	Tyr	Gly	Asp	His	Trp	Arg	Lys	Met	Arg	Arg	
			120					125					130			
ATC	ATG	ACG	GTG	CCC	TTC	TTC	ACC	AAC	AAG	GTG	GTG	GCG	CAG	AAC	CGC	489
Ile	Met	Thr	Val	Pro	Phe	Phe	Thr	Asn	Lys	Val	Val	Ala	Gln	Asn	Arg	
			135					140				145				
GTG	GGG	TGG	GAG	GAG	GAG	GCC	CGG	CTG	GTG	GTG	GAG	GAC	CTC	AAG	GCC	537
Val	Gly	Trp	Glu	Glu	Glu	Ala	Arg	Leu	Val	Val	Glu	Asp	Leu	Lys	Ala	
		150					155					160				

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GAC CCG GCG GCG GCG ACG GCG GGC GTG GTG GTC CGC CGC AGG CTG CAG Asp Pro Ala Ala Ala Thr Ala Gly Val Val Val Arg Arg Arg Leu Gln 165 170 175	585
CTC ATG ATG TAC AAC GAC ATG TTC CGC ATC ATG TTC GAC CGC CGG TTC Leu Met Met Tyr Asn Asp Met Phe Arg Ile Met Phe Asp Arg Arg Phe 180 185 190 195	633
GAG AGC GTG GCC GAC CCG CTC TTC AAC CAG CTC AAG GCG CTC AAC GCC Glu Ser Val Ala Asp Pro Leu Phe Asn Gln Leu Lys Ala Leu Asn Ala 200 205 210	681
GAG CGC AGC ATC CTC TCC CAG AGC TTC GAC TAC AAC TAC GGC GAC TTC Glu Arg Ser Ile Leu Ser Gln Ser Phe Asp Tyr Asn Tyr Gly Asp Phe 215 220 225	729
ATC CCC GTC CTC CGC CCC TTC CTC CGC CGC TAC CTC AAC CGC TGC ACC Ile Pro Val Leu Arg Pro Phe Leu Arg Arg Tyr Leu Asn Arg Cys Thr 230 235 240	777
AAC CTC AAG ACC AAG CCG ATG AAG GTG TTC GAG GAC CAC TTC GTC CAG Asn Leu Lys Thr Lys Arg Met Lys Val Phe Glu Asp His Phe Val Gln 245 250 255	825
CAG CGC AAG GAG GCG TTG GAG AAG ACG GGT GAG ATC AGG TGC GCC ATG Gln Arg Lys Glu Ala Leu Lys Thr Gly Glu Ile Arg Cys Ala Met 260 265 270 275	873
GAC CAC ATC CTG GAA GCC GAA AGG AAG GGC GAG ATC AAC CAC GAC AAC Asp His Ile Leu Glu Ala Glu Arg Lys Gly Glu Ile Asn His Asp Asn 280 285 290	921
GTC CTC TAC ATC GTC GAG AAC ATC AAC GTC GCA GCC ATC GAG ACG ACG Val Leu Tyr Ile Val Glu Asn Ile Asn Val Ala Ala Ile Glu Thr Thr 295 300 305	969
CTG TGG TCG ATC GAG TGG GGC CTC GCG GAG CTG GTG AAC CAC CCG GAG Leu Trp Ser Ile Glu Trp Gly Leu Ala Glu Leu Val Asn His Pro Glu 310 315 320	1017
ATC CAG CAG AAG CTG CGC GAG GAG ATC GTC GCC GTT CTG GCC GCC GCC Ile Gln Gln Lys Leu Arg Glu Glu Ile Val Ala Val Leu Gly Ala Gly 325 330 335	1065
GTG GCG GTG ACG GAG CCG GAC CTG GAG CCG CTC CCC TAC CTG CAG TCC Val Ala Val Thr Glu Pro Asp Leu Glu Arg Leu Pro Tyr Leu Gln Ser 340 345 350 355	1113
GTG GTG AAG GAG ACG CTC CGC CTC CGC ATG GCA ATC CCG CTC CTG GTG Val Val Lys Glu Thr Leu Arg Leu Arg Met Ala Ile Pro Leu Leu Val 360 365 370	1161
CCG CAC ATG AAC CTC AGC GAC GCC AAG CTC GCC GGC TAC GAC ATC CCC Pro His Met Asn Leu Ser Asp Ala Lys Leu Ala Gly Tyr Asp Ile Pro 375 380 385	1209
GCC GAG TCC AAG ATC CTC GTC AAC GCC TGG TTC CTC GCC AAC GAC CCC Ala Glu Ser Lys Ile Leu Val Asn Ala Trp Phe Leu Ala Asn Asp Pro 390 395 400	1257
AAG CGG TGG GTG CGC GCC GAT GAG TTC AGG CCG GAG AGG TTC CTC GAG Lys Arg Trp Val Arg Ala Asp Glu Phe Arg Pro Glu Arg Phe Leu Glu 405 410 415	1305
GAG GAG AAG GCC GTC GAG GCC CAC GGC AAC GAT TTC CGG TTC GTG CCC Glu Glu Lys Ala Val Glu Ala His Gly Asn Asp Phe Arg Phe Val Pro 420 425 430 435	1353

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TTC GGC GTC GGC CGC CGG AGC TGC CCC GGG ATC ATC CTC GCG CTG CCC Phe Gly Val Gly Arg Arg Ser Cys Pro Gly Ile Ile Leu Ala Leu Pro 440 445 450	1401
ATC ATC GGC ATC ACG CTC GGA CGC CTG GTG CAG AAC TTC CAG CTG CTG Ile Ile Gly Ile Thr Leu Gly Arg Leu Val Gln Asn Phe Gln Leu Leu 455 460 465	1449
CCG CCG CCG GGG CAG GAC AAG ATC GAC ACC ACC GAG AAG CCC GGG CAG Pro Pro Pro Gly Gln Asp Lys Ile Asp Thr Thr Glu Lys Pro Gly Gln 470 475 480	1497
TTT ACC AAC CAG ATC CTC AAG CAC GCC ACC ATT GTC TGC AAG CCA CTC Phe Thr Asn Gln Ile Leu Lys His Ala Thr Ile Val Cys Lys Pro Leu 485 490 495	1545
GAG GCT TAACTGAATT GAGGTTTCGG TCATGGGCGC CCGCTGACGC GGGGAGATGG Glu Ala 500	1601
ATCTATGCAT GTGACTGTGT ATTTTGCCTT CTTTCTTTTT GGTGTGTTT TTTGCAGTAG	1661
TAAGTTTAAT TTTTCTTTGG TGTTGGCCTA TTTGTCTTCA TGTGAGGCGT CGTGTGTGAA	1721
ATTTCCATAT AGTTGGCAAT GTGATGTAAA ACTTGGCTCC AAAAAAAAAA AAAAAAACT	1781
CGAGACTCTT CTCTCTCTCT CTCTCTCTCC AGCCTCGGGT CTCTGCTGGC AAGGGAACCT	1841
GCATTACCCCT GTGTACGACG GCGCCATGTT CGTCCCTGAA GCACCCCTCCC TGCAGAGCTC	1901
CCAGGACAAC TTCGCTGCAT CTGCTGGTTT CAAGCGTCGA AGGAGAGAGT TTTGAATACC	1961
CGAAAGAATA TAGCGTTGGA CATATCTGTC AAACAGGGGA TCTTGCTGTG GGTCTCTTGG	2021
TGGGCCAAAT CGCATAGACA ATCATTCAAA TGGATGGGTT CTTGCTGGT CGGTCAAAAA	2081
GTATATGTTG TAATTGTACG CCTTTTTTGG GTCTTGTTGC CAAAGATCAT GGTATTGAG	2141
TTGTGAGCTC TGAGATAACA GGTGTGTGTA TAGTGAAATA AAGAGGAGCG TCGTCAACAC	2201
CATGTACTAT ATAGGCTTTG AAATTCCATT AAGATGCATC AGAAATCAAT GTTGGATTTG	2261

005777 "46577760

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATATATGGAT CCATGGACGT CCTCCTCCTG GAGAAGGC

38

## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATATATGGAT CCATGGATGT TTTGTTGTTG GAGAAGGCC TCCTGGGCCT CTTCGC

56

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

005111-11500

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATATATGGAT CCATGGATGT TTTGTTGTTG GAAAAAGCTT TGTGGGGTTT GTTCGCCGCG	60
GCGGTGCTGG C	71

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATATATGGAT CCATGGATGT TTTGTTGTTG GAAAAAGCTT TGTGGGGTTT GTTGCTGCT	60
GCTGTTTTGG CTATTGCTGT TGCTAAATTG ACTGGTAAAA GATTAGATT GCCACCAGGT	120
CCATCCGGCG CCCCCATCGT CGG	143

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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TATATAGAAT TCCAGTTAAG CCTCGAGTGG CTTGCAGAC

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1506 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

09713794.11500

ATG Met 1	GAT Asp	GTT Val	TTG Leu	TTG Leu	TTG Leu	GAG Glu	AAG Lys	GCC Ala	CTC Leu	CTG Leu	GGC Gly	CTC Leu	TTC Phe	GCC Ala	GCG Ala	48
5									10					15		
GCG Ala	GTG Val	CTG Leu	GCC Ala	ATC Ile	GCC Ala	GTC Val	GCC Ala	AAG Lys	CTC Leu	ACC Thr	GGC Gly	AAG Lys	CGC Arg	TTC Phe	GCG Arg	96
20								25					30			
CTC Leu	CCC Pro	CCT Pro	GGC Gly	CCC Pro	TCC Ser	GGC Gly	GCC Ala	CCC Pro	ATC Ile	GTC Val	GGC Gly	AAC Asn	TGG Trp	CTG Leu	CAG Gln	144
35						40						45				
GTC Val	GGC Gly	GAC Asp	GAC Asp	CTC Leu	AAC Asn	CAC His	CGC Arg	AAC Asn	CTG Leu	ATG Met	GGC Gly	CTG Leu	GCC Ala	AAG Lys	GCG Arg	192
50						55					60					
TTC Phe	GGC Gly	GAG Glu	GTG Val	TTT Phe	CTC Leu	CTC Leu	CGC Arg	ATG Met	GGC Gly	GTC Val	CGC Arg	AAC Asn	CTG Leu	GTG Val	GTC Val	240
65					70					75					80	
GTC Val	TCC Ser	AGC Ser	CCC Pro	GAG Glu	CTC Leu	GCC Ala	AAG Lys	GAG Glu	GTC Val	CTC Leu	CAC His	ACC Thr	CAG Gln	GGC Gly	GTC Val	288
				85				90					95			
GAG Glu	TTC Phe	GGC Gly	TCC Ser	CGC Arg	ACC Thr	CGC Arg	AAC Asn	GTC Val	GTC Val	TTC Phe	GAC Asp	ATC Ile	TTC Phe	ACC Thr	GCG Gly	336
			100					105					110			
AAG Lys	GGA Gly	CAG Gln	GAC Asp	ATG Met	GTG Val	TTT Phe	ACG Thr	GTG Val	TAC Tyr	GGC Gly	GAC Asp	CAC His	TGG Trp	CGC Arg	AAG Lys	384
		115					120					125				
ATG Met	CGG Arg	CGG Arg	ATC Ile	ATG Met	ACG Thr	GTG Val	CCC Pro	TTC Phe	TTC Phe	ACC Thr	AAC Asn	AAG Lys	GTG Val	GTG Val	GCG Ala	432
	130					135					140					
CAG Gln	AAC Asn	CGC Arg	GTG Val	GGG Gly	TGG Trp	GAG Glu	GAG Glu	GAG Glu	GCC Ala	CGG Arg	CTG Leu	GTG Val	GTG Val	GAG Glu	GAC Asp	480
	145				150					155					160	
CTC Leu	AAG Lys	GCC Ala	GAC Asp	CCG Pro	GCG Ala	GCG Ala	GCG Ala	ACG Thr	GCG Ala	GGC Gly	GTG Val	GTG Val	GTC Val	CGC Arg	CGC Arg	528
				165				170						175		
AGG Arg	CTG Leu	CAG Gln	CTC Leu	ATG Met	ATG Met	TAC Tyr	AAC Asn	GAC Asp	ATG Met	TTC Phe	CGC Arg	ATC Ile	ATG Met	TTC Phe	GAC Asp	576
			180					185					190			
CGC Arg	CGG Arg	TTC Phe	GAG Glu	AGC Ser	GTG Val	GCC Ala	GAC Asp	CCG Pro	CTC Leu	TTC Phe	AAC Asn	CAG Gln	CTC Leu	AAG Lys	GCG Ala	624
		195					200					205				
CTC Leu	AAC Asn	GCC Ala	GAG Glu	CGC Arg	AGC Ser	ATC Ile	CTC Leu	TCC Ser	CAG Gln	AGC Ser	TTC Phe	GAC Asp	TAC Tyr	AAC Asn	TAC Tyr	672
	210					215					220					
GGC Gly	GAC Asp	TTC Phe	ATC Ile	CCC Pro	GTC Val	CTC Leu	CGC Arg	CCC Pro	TTC Phe	CTC Leu	CGC Arg	CGC Arg	TAC Tyr	CTC Leu	AAC Asn	720
	225				230					235					240	

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CGC	TGC	ACC	AAC	CTC	AAG	ACC	AAG	CGG	ATG	AAG	GTG	TTC	GAG	GAC	CAC	768
Arg	Cys	Thr	Asn	Leu	Lys	Thr	Lys	Arg	Met	Lys	Val	Phe	Glu	Asp	His	
			245						250					255		
TTC	GTC	CAG	CAG	CGC	AAG	GAG	CGG	TTG	GAG	AAG	ACG	GGT	GAG	ATC	AGG	816
Phe	Val	Gln	Gln	Arg	Lys	Glu	Ala	Leu	Glu	Lys	Thr	Gly	Glu	Ile	Arg	
			260					265					270			
TGC	GCC	ATG	GAC	CAC	ATC	CTG	GAA	GCC	GAA	AGG	AAG	GGC	GAG	ATC	AAC	864
Cys	Ala	Met	Asp	His	Ile	Leu	Glu	Ala	Glu	Arg	Lys	Gly	Glu	Ile	Asn	
		275					280					285				
CAC	GAC	AAC	GTC	CTC	TAC	ATC	GTC	GAG	AAC	ATC	AAC	GTC	GCA	GCC	ATC	912
His	Asp	Asn	Val	Leu	Tyr	Ile	Val	Glu	Asn	Ile	Asn	Val	Ala	Ala	Ile	
	290					295					300					
GAG	ACG	ACG	CTG	TGG	TGC	ATC	GAG	TGG	GGC	CTC	GCG	GAG	CTG	GTG	AAC	960
Glu	Thr	Thr	Leu	Trp	Ser	Ile	Glu	Trp	Gly	Leu	Ala	Glu	Leu	Val	Asn	
305					310				315					320		
CAC	CCG	GAG	ATC	CAG	CAG	AAG	CTG	CGC	GAG	GAG	ATC	GTC	GCC	GTT	CTG	1008
His	Pro	Glu	Ile	Gln	Gln	Lys	Leu	Arg	Glu	Glu	Ile	Val	Ala	Val	Leu	
				325					330					335		
GGC	GCC	GGC	GTG	GCG	GTG	ACG	GAG	CCG	GAC	CTG	GAG	CGC	CTC	CCC	TAC	1056
Gly	Ala	Gly	Val	Ala	Val	Thr	Glu	Pro	Asp	Leu	Glu	Arg	Leu	Pro	Tyr	
			340					345					350			
CTG	CAG	TCC	GTG	GTG	AAG	GAG	ACG	CTC	CGC	CTC	CGC	ATG	GCA	ATC	CCG	1104
Leu	Gln	Ser	Val	Val	Lys	Glu	Thr	Leu	Arg	Leu	Arg	Met	Ala	Ile	Pro	
		355					360					365				
CTC	CTG	GTG	CCG	CAC	ATG	AAC	CTC	AGC	GAC	GCC	AAG	CTC	GCC	GGC	TAC	1152
Leu	Leu	Val	Pro	His	Met	Asn	Leu	Ser	Asp	Ala	Lys	Leu	Ala	Gly	Tyr	
		370				375					380					
GAC	ATC	CCC	GCC	GAG	TCC	AAG	ATC	CTC	GTC	AAC	GCC	TGG	TTC	CTC	GCC	1200
Asp	Ile	Pro	Ala	Glu	Ser	Lys	Ile	Leu	Val	Asn	Ala	Trp	Phe	Leu	Ala	
385					390					395					400	
AAC	GAC	CCC	AAG	CGG	TGG	GTG	CGC	GCC	GAT	GAG	TTC	AGG	CCG	GAG	AGG	1248
Asn	Asp	Pro	Lys	Arg	Trp	Val	Arg	Ala	Asp	Glu	Phe	Arg	Pro	Glu	Arg	
				405					410					415		
TTC	CTC	GAG	GAG	GAG	AAG	GCC	GTC	GAG	GCC	CAC	GGC	AAC	GAT	TTC	CGG	1296
Phe	Leu	Glu	Glu	Glu	Lys	Ala	Val	Glu	Ala	His	Gly	Asn	Asp	Phe	Arg	
			420					425					430			
TTC	GTG	CCC	TTC	GGC	GTC	GGC	CGC	CGG	AGC	TGC	CCC	GGG	ATC	ATC	CTC	1344
Phe	Val	Pro	Phe	Gly	Val	Gly	Arg	Arg	Ser	Cys	Pro	Gly	Ile	Ile	Leu	
		435					440					445				
GGC	CTG	CCC	ATC	ATC	GGC	ATC	ACG	CTC	GGA	CGC	CTG	GTG	CAG	AAC	TTC	1392
Ala	Leu	Pro	Ile	Ile	Gly	Ile	Thr	Leu	Gly	Arg	Leu	Val	Gln	Asn	Phe	
		450				455					460					
CAG	CTG	CTG	CCG	CCG	CCG	GGG	CAG	GAC	AAG	ATC	GAC	ACC	ACC	GAG	AAG	1440
Gln	Leu	Leu	Pro	Pro	Pro	Gly	Gln	Asp	Lys	Ile	Asp	Thr	Thr	Glu	Lys	
465					470				475						480	
CCC	GGG	CAG	TTT	ACC	AAC	CAG	ATC	CTC	AAG	CAC	GCC	ACC	ATT	GTC	TGC	1488
Pro	Gly	Gln	Phe	Thr	Asn	Gln	Ile	Leu	Lys	His	Ala	Thr	Ile	Val	Cys	
				485					490					495		
AAG	CCA	CTC	GAG	GCT	TAA											1506
Lys	Pro	Leu	Glu	Ala												
				500												

005777 16272650

## (2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1506 base pairs
  - (B) TYPE: nucleotide
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..1503
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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ATG Met 1	GAT Asp	GTT Val	TTG Leu	TTG Leu	TTG Leu	GAA Glu	AAA Lys	GCT Ala	TTG Leu	TTG Leu	GGT Gly	TTG Leu	TTC Phe	GCC Ala	GCG Ala	48
5									10					15		
GCG Ala	GTG Val	CTG Leu	GCC Ala	ATC Ile	GCC Ala	GTC Val	GCC Ala	AAG Lys	CTC Leu	ACC Thr	GGC Gly	AAG Lys	CGC Arg	TTC Phe	GCG Arg	96
20								25					30			
CTC Leu	CCC Pro	CCT Pro	GGC Gly	CCC Pro	TCC Ser	GGC Gly	GCC Ala	CCC Pro	ATC Ile	GTC Val	GGC Gly	AAC Asn	TGG Trp	CTG Leu	CAG Gln	144
35							40					45				
GTC Val	GGC Gly	GAC Asp	GAC Asp	CTC Leu	AAC Asn	CAC His	CGC Arg	AAC Asn	CTG Leu	ATG Met	GGC Gly	CTG Leu	GCC Ala	AAG Lys	GCG Arg	192
50						55					60					
TTC Phe	GGC Gly	GAG Glu	GTG Val	TTC Phe	CTC Leu	CTC Leu	CGC Arg	ATG Met	GGC Gly	GTC Val	CGC Arg	AAC Asn	CTG Leu	GTG Val	GTC Val	240
65					70				75					80		
GTC Val	TCC Ser	AGC Ser	CCC Pro	GAG Glu	CTC Leu	GCC Ala	AAG Lys	GAG Glu	GTC Val	CTC Leu	CAC His	ACC Thr	CAG Gln	GGC Gly	GTC Val	288
				85				90					95			
GAG Glu	TTC Phe	GGC Gly	TCC Ser	CGC Arg	ACC Thr	CGC Arg	AAC Asn	GTC Val	GTC Val	TTC Phe	GAC Asp	ATC Ile	TTC Phe	ACC Thr	GGC Gly	336
			100					105					110			
AAG Lys	GGA Gly	CAG Gln	GAC Asp	ATG Met	GTG Val	TTC Phe	ACG Thr	GTG Val	TAC Tyr	GGC Gly	GAC Asp	CAC His	TGG Trp	CGC Arg	AAG Lys	384
		115					120					125				
ATG Met	CGG Arg	CGG Arg	ATC Ile	ATG Met	ACG Thr	GTG Val	CCC Pro	TTC Phe	TTC Phe	ACC Thr	AAC Asn	AAG Lys	GTG Val	GTG Val	GCG Ala	432
	130					135						140				
CAG Gln	AAC Asn	CGC Arg	GTG Val	GGG Gly	TGG Trp	GAG Glu	GAG Glu	GAG Glu	GCC Ala	CGG Arg	CTG Leu	GTG Val	GTG Val	GAG Glu	GAC Asp	480
145				150					155					160		
CTC Leu	AAG Lys	GCC Ala	GAC Asp	CCG Pro	GCG Ala	GCG Ala	GCG Ala	ACG Thr	GCG Ala	GGC Gly	GTG Val	GTG Val	GTC Val	CGC Arg	CGC Arg	528
				165				170					175			
AGG Arg	CTG Leu	CAG Gln	CTC Leu	ATG Met	ATG Met	TAC Tyr	AAC Asn	GAC Asp	ATG Met	TTC Phe	CGC Arg	ATC Ile	ATG Met	TTC Phe	GAC Asp	576
			180					185					190			
CGC Arg	CGG Arg	TTC Phe	GAG Glu	AGC Ser	GTG Val	GCC Ala	GAC Asp	CCG Pro	CTC Leu	TTC Phe	AAC Asn	CAG Gln	CTC Leu	AAG Lys	GCG Ala	624
		195					200					205				

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CTC Leu 210	AAC Asn 210	GCC Ala 210	GAG Glu 210	CGC Arg 210	AGC Ser 215	ATC Ile 215	CTC Leu 215	TCC Ser 215	CAG Gln 215	AGC Ser 220	TTC Phe 220	GAC Asp 220	TAC Tyr 220	AAC Asn 220	TAC Tyr 220	672
GGC Gly 225	GAC Asp 225	TTC Phe 225	ATC Ile 225	CCC Pro 230	GTC Val 230	CTC Leu 230	CGC Arg 230	CCC Pro 235	TTC Phe 235	CTC Leu 235	CGC Arg 235	CGC Arg 235	TAC Tyr 235	CTC Leu 240	AAC Asn 240	720
CGC Arg 245	TGC Cys 245	ACC Thr 245	AAC Asn 245	CTC Leu 245	AAG Lys 245	ACC Thr 245	AAG Lys 245	CGG Arg 250	ATG Met 250	AAG Lys 250	GTG Val 250	TTC Phe 255	GAG Glu 255	GAC Asp 255	CAC His 255	768
TTC Phe 260	GTC Val 260	CAG Gln 260	CAG Gln 260	CGC Arg 260	AAG Lys 260	GAG Glu 265	GGC Ala 265	TTG Leu 265	GAG Glu 265	AAG Lys 265	ACG Thr 270	GGT Gly 270	GAG Glu 270	ATC Ile 270	AGG Arg 270	816
TGC Cys 275	GCC Ala 275	ATG Met 275	GAC Asp 275	CAC His 280	ATC Ile 280	CTG Leu 280	GAA Glu 280	GCC Ala 280	GAA Glu 285	AGG Arg 285	AAG Lys 285	GGC Gly 285	GAG Glu 285	ATC Ile 285	AAC Asn 285	864
CAC His 290	GAC Asp 290	AAC Asn 290	GTC Val 290	CTC Leu 295	TAC Tyr 295	ATC Ile 295	GTC Val 295	GAG Glu 300	AAC Asn 300	ATC Ile 300	AAC Asn 300	GTC Val 300	GCA Ala 300	GCC Ala 300	ATC Ile 300	912
GAG Glu 305	ACG Thr 305	ACG Thr 305	CTG Leu 310	TGG Trp 310	TGG Trp 310	ATC Ile 310	GAG Glu 310	TGG Trp 315	GGC Gly 315	CTC Leu 315	GCG Ala 315	GAG Glu 315	CTG Leu 320	GTG Val 320	AAC Asn 320	960
CAC His 325	CCG Pro 325	GAG Glu 325	ATC Ile 325	CAG Gln 325	CAG Gln 325	AAG Lys 325	CTG Leu 330	CGC Arg 330	GAG Glu 330	GAG Glu 330	ATC Ile 330	GTC Val 335	GCC Ala 335	GTT Val 335	CTG Leu 335	1008
GGC Gly 340	GCC Ala 340	GGC Gly 340	GTG Val 340	GCG Ala 340	GTG Val 340	ACG Thr 345	GAG Glu 345	CCG Pro 345	GAC Asp 345	CTG Leu 350	GAG Glu 350	CGC Arg 350	CTC Leu 350	CCC Pro 350	TAC Tyr 350	1056
CTG Leu 355	CAG Gln 355	TCC Ser 355	GTG Val 355	GTG Val 355	AAG Lys 360	GAG Glu 360	ACG Thr 360	CTC Leu 360	CGC Arg 365	CTC Leu 365	CGC Arg 365	ATG Met 365	GCA Ala 365	ATC Ile 365	CCG Pro 365	1104
CTC Leu 370	CTG Leu 370	GTG Val 370	CCG Pro 375	CAC His 375	ATG Met 375	AAC Asn 375	CTC Leu 375	AGC Ser 380	GAC Asp 380	GCC Ala 380	AAG Lys 380	CTC Leu 380	GCC Ala 380	GGC Ala 380	TAC Tyr 380	1152
GAC Asp 385	ATC Ile 385	CCC Pro 390	GCC Ala 390	GAG Glu 390	TCC Ser 390	AAG Lys 390	ATC Ile 395	CTC Leu 395	GTC Val 395	AAC Asn 395	GCC Ala 395	TGG Trp 400	TTC Phe 400	CTC Leu 400	GCC Ala 400	1200
AAC Asn 405	GAC Asp 405	CCC Pro 405	AAG Lys 405	CGG Arg 405	TGG Trp 410	GTG Val 410	CGC Arg 410	GCC Ala 410	GAT Asp 410	GAG Glu 415	TTC Phe 415	AGG Arg 415	CCG Pro 415	GAG Glu 415	AGG Arg 415	1248
TTC Phe 420	CTC Leu 420	GAG Glu 420	GAG Glu 420	AAG Lys 420	GCC Ala 425	GTC Val 425	GAG Glu 425	GCC Ala 425	CAC His 430	GGC Gly 430	AAC Asn 430	GAT Asp 430	TTC Phe 430	CGG Arg 430	1296	
TTC Phe 435	GTG Val 435	CCC Pro 435	TTC Phe 435	GGC Gly 440	GTC Val 440	GGC Gly 440	CGC Arg 440	CGG Arg 440	AGC Ser 445	TGC Cys 445	CCC Pro 445	GGG Gly 445	ATC Ile 445	ATC Ile 445	CTC Leu 445	1344
GGC Ala 450	CTG Leu 450	CCC Pro 450	ATC Ile 450	ATC Ile 450	GGC Gly 455	ATC Ile 455	ACG Thr 455	CTC Leu 455	GGA Gly 460	CGC Arg 460	CTG Leu 460	GTG Val 460	CAG Gln 460	AAC Asn 460	TTC Phe 460	1392
CAG Gln 465	CTG Leu 465	CTG Leu 465	CCG Pro 465	CCG Pro 465	CCG Pro 470	GGG Gly 470	CAG Gln 470	GAC Asp 475	AAG Lys 475	ATC Ile 475	GAC Asp 475	ACC Thr 475	ACC Thr 475	GAG Glu 480	AAG Lys 480	1440

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CCC GGG CAG TTT ACC AAC CAG ATC CTC AAG CAC GCC ACC ATT GTC TGC	1488
Pro Gly Gln Phe Thr Asn Gln Il Leu Lys His Ala Thr Ile Val Cys	
485 490 495	
AAG CCA CTC GAG GCT TAA	1506
Lys Pro Leu Glu Ala	
500	

## (2) INFORMATION FOR SEQ ID NO: 9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1506 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1503

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

09713794.11500

ATG	GAT	GTT	TTG	TTG	TTG	GAA	AAA	GCT	TTG	TTG	GGT	TTG	TTT	GCT	GCT	48
Met	Asp	Val	Leu	Leu	Leu	Glu	Lys	Ala	Leu	Leu	Gly	Leu	Phe	Ala	Ala	
			505					510					515			
GCT	GTT	TTG	GCT	ATT	GCT	GTT	GCT	AAA	TTG	ACT	GGT	AAA	AGA	TTT	AGA	96
Ala	Val	Leu	Ala	Ile	Ala	Val	Ala	Lys	Leu	Thr	Gly	Lys	Arg	Phe	Arg	
		520					525					530				
TTG	CCA	CCA	GGT	CCA	TCC	GGC	GCC	CCC	ATC	GTC	GGC	AAC	TGG	CTG	CAG	144
Leu	Pro	Pro	Gly	Pro	Ser	Gly	Ala	Pro	Ile	Val	Gly	Asn	Trp	Leu	Gln	
		35					40					45				
GTC	GGC	GAC	GAC	CTC	AAC	CAC	CGC	AAC	CTG	ATG	GGC	CTG	GCC	AAG	CGG	192
Val	Gly	Asp	Asp	Leu	Asn	His	Arg	Asn	Leu	Met	Gly	Leu	Ala	Lys	Arg	
		50				55					60					
TTC	GGC	GAG	GTG	TTC	CTC	CTC	CGC	ATG	GGC	GTC	CGC	AAC	CTG	GTG	GTC	240
Phe	Gly	Glu	Val	Phe	Leu	Leu	Arg	Met	Gly	Val	Arg	Asn	Leu	Val	Val	
	65				70					75					80	
GTC	TCC	AGC	CCC	GAG	CTC	GCC	AAG	GAG	GTC	CTC	CAC	ACC	CAG	GGC	GTC	288
Val	Ser	Ser	Pro	Glu	Leu	Ala	Lys	Glu	Val	Leu	His	Thr	Gln	Gly	Val	
				85					90					95		
GAG	TTC	GGC	TCC	CGC	ACC	CGC	AAC	GTC	GTC	TTC	GAC	ATC	TTC	ACC	GGC	336
Glu	Phe	Gly	Ser	Arg	Thr	Arg	Asn	Val	Val	Phe	Asp	Ile	Phe	Thr	Gly	
			100					105					110			
AAG	GGA	CAG	GAC	ATG	GTG	TTC	ACG	GTG	TAC	GGC	GAC	CAC	TGG	CGC	AAG	384
Lys	Gly	Gln	Asp	Met	Val	Phe	Thr	Val	Tyr	Gly	Asp	His	Trp	Arg	Lys	
		115					120					125				
ATG	CGG	CGG	ATC	ATG	ACG	GTG	CCC	TTC	TTC	ACC	AAC	AAG	GTG	GTG	CGC	432
Met	Arg	Arg	Ile	Met	Thr	Val	Pro	Phe	Phe	Thr	Asn	Lys	Val	Val	Ala	
		130				135					140					
CAG	AAC	CGC	GTG	GGG	TGG	GAG	GAG	GAG	GCC	CGG	CTG	GTG	GTG	GAG	GAC	480
Gln	Asn	Arg	Val	Gly	Trp	Glu	Glu	Glu	Ala	Arg	Leu	Val	Val	Glu	Asp	
	145				150					155					160	
CTC	AAG	GCC	GAC	CCG	GCG	GCG	GCG	ACG	GCG	GGC	GTG	GTG	GTC	CGC	CGC	528
Leu	Lys	Ala	Asp	Pro	Ala	Ala	Ala	Thr	Ala	Gly	Val	Val	Val	Arg	Arg	
				165					170					175		

005TTT 462ET 60

AGG	CTG	CAG	CTC	ATG	ATG	TAC	AAC	GAC	ATG	TTC	CGC	ATC	ATG	TTC	GAC	576
Arg	Leu	Gln	Leu	Met	Met	Tyr	Asn	Asp	Met	Phe	Arg	Ile	Met	Phe	Asp	
			180					185								
CGC	CGG	TTC	GAG	AGC	GTG	GCC	GAC	CCG	CTC	TTC	AAC	CAG	CTC	AAG	GCG	624
Arg	Arg	Phe	Glu	Ser	Val	Ala	Asp	Pro	Leu	Phe	Asn	Gln	Leu	Lys	Ala	
		195					200					205				
CTC	AAC	GCC	GAG	CGC	AGC	ATC	CTC	TCC	CAG	AGC	TTC	GAC	TAC	AAC	TAC	672
Leu	Asn	Ala	Glu	Arg	Ser	Ile	Leu	Ser	Gln	Ser	Phe	Asp	Tyr	Asn	Tyr	
	210					215					220					
GGC	GAC	TTC	ATC	CCC	GTG	CTC	CGC	CCC	TTC	CTC	CGC	CGC	TAC	CTC	AAC	720
Gly	Asp	Phe	Ile	Pro	Val	Leu	Arg	Pro	Phe	Leu	Arg	Arg	Tyr	Leu	Asn	
	225				230					235					240	
CGC	TGC	ACC	AAC	CTC	AAG	ACC	AAG	CGG	ATG	AAG	GTG	TTC	GAG	GAC	CAC	768
Arg	Cys	Thr	Asn	Leu	Lys	Thr	Lys	Arg	Met	Lys	Val	Phe	Glu	Asp	His	
			245					250						255		
TTC	GTC	CAG	CAG	CGC	AAG	GAG	GCG	TTG	GAG	AAG	ACG	GGT	GAG	ATC	AGG	815
Phe	Val	Gln	Gln	Arg	Lys	Glu	Ala	Leu	Glu	Lys	Thr	Gly	Glu	Ile	Arg	
			260					265					270			
TGC	GCC	ATG	GAC	CAC	ATC	CTG	GAA	GCC	GAA	AGG	AAG	GGC	GAG	ATC	AAC	864
Cys	Ala	Met	Asp	His	Ile	Leu	Glu	Ala	Glu	Arg	Lys	Gly	Glu	Ile	Asn	
		275					280					285				
CAC	GAC	AAC	GTC	CTC	TAC	ATC	GTC	GAG	AAC	ATC	AAC	GTC	GCA	GCC	ATC	912
His	Asp	Asn	Val	Leu	Tyr	Ile	Val	Glu	Asn	Ile	Asn	Val	Ala	Ala	Ile	
	290					295					300					
GAG	ACG	ACG	CTG	TGG	TCG	ATC	GAG	TGG	GGC	CTC	GCG	GAG	CTG	GTG	AAC	960
Glu	Thr	Thr	Leu	Trp	Ser	Ile	Glu	Trp	Gly	Leu	Ala	Glu	Leu	Val	Asn	
	305				310				315						320	
CAC	CCG	GAG	ATC	CAG	CAG	AAG	CTG	CGC	GAG	GAG	ATC	GTC	GCC	GTT	CTG	1008
His	Pro	Glu	Ile	Gln	Lys	Leu	Arg	Glu	Glu	Ile	Val	Ala	Ala	Val	Leu	
				325				330						335		
GGC	GCC	GGC	GTG	GCG	GTG	ACG	GAG	CCG	GAC	CTG	GAG	CGC	CTC	CCC	TAC	1056
Gly	Ala	Gly	Val	Ala	Val	Thr	Glu	Pro	Asp	Leu	Glu	Arg	Leu	Pro	Tyr	
			340					345					350			
CTG	CAG	TCC	GTG	GTG	AAG	GAG	ACG	CTC	CGC	CTC	CGC	ATG	GCA	ATC	CCG	1104
Leu	Gln	Ser	Val	Val	Lys	Glu	Thr	Leu	Arg	Leu	Arg	Met	Ala	Ile	Pro	
		355					360					365				
CTC	CTG	GTG	CCG	CAC	ATG	AAC	CTC	AGC	GAC	GCC	AAG	CTC	GCC	GGC	TAC	1152
Leu	Leu	Val	Pro	His	Met	Asn	Leu	Ser	Asp	Ala	Lys	Leu	Ala	Gly	Tyr	
		370				375					380					
GAC	ATC	CCC	GCC	GAG	TCC	AAG	ATC	CTC	GTC	AAC	GCC	TGG	TTC	CTC	GCC	1200
Asp	Ile	Pro	Ala	Glu	Ser	Lys	Ile	Leu	Val	Asn	Ala	Trp	Phe	Leu	Ala	
					390					395					400	
AAC	GAC	CCC	AAG	CGG	TGG	GTG	CGC	GCC	GAT	GAG	TTC	AGG	CCG	GAG	AGG	1248
Asn	Asp	Pro	Lys	Arg	Trp	Val	Arg	Ala	Asp	Glu	Phe	Arg	Pro	Glu	Arg	
				405					410					415		
TTC	CTC	GAG	GAG	GAG	AAG	GCC	GTC	GAG	GCC	CAC	GGC	AAC	GAT	TTC	CGG	1296
Phe	Leu	Glu	Glu	Glu	Lys	Ala	Val	Glu	Ala	His	Gly	Asn	Asp	Phe	Arg	
			420					425					430			
TTC	GTG	CCC	TTC	GGC	GTC	GGC	CGC	CGG	AGC	TGC	CCC	GGG	ATC	ATC	CTC	1344
Phe	Val	Pro	Phe	Gly	Val	Gly	Arg	Arg	Ser	Cys	Pro	Gly	Ile	Ile	Leu	
		435					440					445				

005113794 11500

GCG CTG CCC ATC ATC GGC ATC ACG CTC GGA CGC CTG GTG CAG AAC TTC	1392
Ala Leu Pro Ile Ile Gly Ile Thr Leu Gly Arg Leu Val Gln Asn Phe	
450 455 460	
CAG CTG CTG CCG CCG CCG GGG CAG GAC AAG ATC GAC ACC ACC GAG AAG	1440
Gln Leu Leu Pro Pro Pro Gly Gln Asp Lys Ile Asp Thr Thr Glu Lys	
465 470 475 480	
CCC GGG CAG TTT ACC AAC CAG ATC CTC AAG CAC GCC ACC ATT GTC TGC	1488
Pro Gly Gln Phe Thr Asn Gln Ile Leu Lys His Ala Thr Ile Val Cys	
485 490 495	
AAG CCA CTC GAG GCT TAA	1506
Lys Pro Leu Glu Ala	
500	

## (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2181 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 112..1734

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

09713794.11500



CGATCCACCC CTTGGATCCA CTCTACCCAG CTCGCTAGCC AGCGGGGTAC ATACACGCAC	60
GCACGTACGC GCGTACGTAC ACTCGCAGAG CTTGCTTCAG GGAGGCCGGC A ATG GAG	117
Met Glu	1
GTG GGG ACG TGG GCG GTG GTG GTG TCG GCG GTG GCC GCG TAC ATG GCG	165
Val Gly Thr Trp Ala Val Val Val Ser Ala Val Ala Ala Tyr Met Ala	5 10 15
TGG TTC TGG CCG ATG TCC CGC GGG CTG CGC GGG CCG CCG GTT TGG CCC	213
Trp Phe Trp Arg Met Ser Arg Gly Leu Arg Gly Pro Arg Val Trp Pro	20 25 30
GTG CTC GGC AGC CTG CCG GGC CTG GTG CAG CAC GCC GAG GAC ATG CAC	261
Val Leu Gly Ser Leu Pro Gly Leu Val Gln His Ala Glu Asp Met His	35 40 45 50
GAG TGG ATC GCC GGC AAC CTG CGC CGC GCG GGC GGC ACG TAC CAG ACC	309
Glu Trp Ile Ala Gly Asn Leu Arg Arg Ala Gly Gly Thr Tyr Gln Thr	55 60 65
TGC ATC TTC GCC GTG CCC GGG GTG GCG CGC CGC GGC GGC CTG GTC ACC	357
Cys Ile Phe Ala Val Pro Gly Val Ala Arg Arg Gly Gly Leu Val Thr	70 75 80
GTC ACC TGC GAC CCG CGC AAC CTG GAG CAC GTC CTG AAG GCG CGC TTC	405
Val Thr Cys Asp Pro Arg Asn Leu Glu His Val Leu Lys Ala Arg Phe	85 90 95
GAC AAC TAC CCC AAG GGC CCC TTC TGG CAC GGC GTC TTC CCG GAC CTG	453
Asp Asn Tyr Pro Lys Gly Pro Phe Trp His Gly Val Phe Arg Asp Leu	100 105 110

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CTC	GGC	GAC	GGC	ATC	TTC	AAT	TCC	GAC	GGC	GAC	ACC	TGG	CTC	GGC	CAG	501
Leu	Gly	Asp	Gly	Ile	Phe	Asn	Ser	Asp	Gly	Asp	Thr	Trp	Leu	Ala	Gln	
115					120					125					130	
CGC	AAG	ACG	GCC	GCG	CTC	GAG	TTC	ACC	ACC	CGC	ACG	CTC	CGG	ACG	GCC	549
Arg	Lys	Thr	Ala	Ala	Leu	Glu	Phe	Thr	Thr	Arg	Thr	Leu	Arg	Thr	Ala	
				135					140					145		
ATG	TCC	CGC	TGG	GTC	TCG	CGC	TCC	ATC	CAC	GGC	CGC	CTC	CTG	CCC	ATC	597
Met	Ser	Arg	Trp	Val	Ser	Arg	Ser	Ile	His	Gly	Arg	Leu	Leu	Pro	Ile	
			150					155					160			
CTG	GCC	GAC	GCG	GCC	AAG	GGC	AAG	GCG	CAG	GTG	GAT	CTC	CAG	GAC	CTC	645
Leu	Ala	Asp	Ala	Ala	Lys	Gly	Lys	Ala	Gln	Val	Asp	Leu	Gln	Asp	Leu	
		165					170					175				
CTC	CTC	CGC	CTC	ACC	TTC	GAC	AAC	ATC	TGC	GGC	CTG	GCC	TTC	GGC	AAG	693
Leu	Leu	Arg	Leu	Thr	Phe	Asp	Asn	Ile	Cys	Gly	Leu	Ala	Phe	Gly	Lys	
	180				185						190					
GAC	CCG	GAG	ACG	CTC	GCC	CAG	GGC	CTG	CCG	GAG	AAC	GAG	TTC	GCC	TCC	741
Asp	Pro	Glu	Thr	Leu	Ala	Gln	Gly	Leu	Pro	Glu	Asn	Glu	Phe	Ala	Ser	
195					200					205					210	
GCG	TTC	GAC	CGC	GCC	ACC	GAG	GCC	ACG	CTC	AAC	CGC	TTC	ATC	TTC	CCG	789
Ala	Phe	Asp	Arg	Ala	Thr	Glu	Ala	Thr	Leu	Asn	Arg	Phe	Ile	Phe	Pro	
				215					220					225		
GAG	TTC	CTG	TGG	CGC	TGC	AAA	AAG	TGG	CTG	GGC	CTC	GGC	ATG	GAG	ACC	837
Glu	Phe	Leu	Trp	Arg	Cys	Lys	Lys	Trp	Leu	Gly	Leu	Gly	Met	Glu	Thr	
			230					235					240			
ACG	CTG	ACC	AGC	AGC	ATG	GCC	CAC	GTC	GAC	CAG	TAC	CTC	GCC	GCC	GTC	885
Thr	Leu	Thr	Ser	Ser	Met	Ala	His	Val	Asp	Gln	Tyr	Leu	Ala	Ala	Val	
		245					250					255				
ATC	AAG	AAG	CGC	AAG	CTC	GAG	CTC	GCC	GCC	GGC	AAC	GGC	AAA	TGC	GAC	933
Ile	Lys	Lys	Arg	Lys	Leu	Glu	Leu	Ala	Ala	Gly	Asn	Gly	Lys	Cys	Asp	
	260					265					270					
ACG	GCG	GCG	ACG	CAC	GAC	GAC	CTG	CTC	TCC	CGG	TTC	ATG	CGG	AAG	GGT	981
Thr	Ala	Ala	Thr	His	Asp	Asp	Leu	Leu	Ser	Arg	Phe	Met	Arg	Lys	Gly	
275					280					285					290	
TCC	TAC	TCG	GAC	GAG	TCG	CTC	CAG	CAC	GTG	GCG	CTC	AAC	TTC	ATC	CTC	1029
Ser	Tyr	Ser	Asp	Glu	Ser	Leu	Gln	His	Val	Ala	Leu	Asn	Phe	Ile	Leu	
			295						300					305		
GCC	GGC	CGC	GAC	ACC	TCC	TCC	GTG	GCG	CTC	TCC	TGG	TTC	TTC	TGG	CTC	1077
Ala	Gly	Arg	Asp	Thr	Ser	Ser	Val	Ala	Leu	Ser	Trp	Phe	Phe	Trp	Leu	
			310					315					320			
GTG	TCC	ACC	CAC	CCT	GCG	GTG	GAG	CGC	AAG	ATC	GTG	CGC	GAG	CTC	TGC	1125
Val	Ser	Thr	His	Pro	Ala	Val	Glu	Arg	Lys	Ile	Val	Arg	Glu	Leu	Cys	
		325					330					335				
TCC	GTT	CTC	GCC	GCG	TCA	CGG	GGC	GCC	CAT	GAC	CCG	GCA	TTG	TGG	CTG	1173
Ser	Val	Leu	Ala	Ala	Ser	Arg	Gly	Ala	His	Asp	Pro	Ala	Leu	Trp	Leu	
	340					345					350					
GCG	GAG	CCC	TTC	ACC	TTC	GAG	GAG	CTC	GAC	CGC	CTG	GTC	TAC	CTC	AAG	1221
Ala	Glu	Pro	Phe	Thr	Phe	Glu	Glu	Leu	Asp	Arg	Leu	Val	Tyr	Leu	Lys	
355					360					365					370	
GCG	GCG	CTG	TCG	GAG	ACC	CTC	CGC	CTC	TAC	CCC	TCC	GTC	CCC	GAG	GAC	1269
Ala	Ala	Leu	Ser	Glu	Thr	Leu	Arg	Leu	Tyr	Pro	Ser	Val	Pro	Glu	Asp	
				375					380					385		

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TCC AAG CAC GTC GTC GCG GAC GAC TAC CTC CCC GAC GGC ACC TTC GTG Ser Lys His Val Val Ala Asp Asp Tyr Leu Pro Asp Gly Thr Phe Val 390 395 400	1317
CCG GCC GGG TCG TCG GTC ACC TAC TCC ATA TAC TCG GCG GGG CGC ATG Pro Ala Gly Ser Ser Val Thr Tyr Ser Ile Tyr Ser Ala Gly Arg Met 405 410 415	1365
AAG GGG GTG TGG GGG GAG GAC TGC CTC GAG TTC CCG CCG GAG CGA TGG Lys Gly Val Trp Gly Glu Asp Cys Leu Glu Phe Arg Pro Glu Arg Trp 420 425 430	1413
CTG TCG GCC GAC GGC ACC AAG TTC GAG CAG CAC GAC TCG TAC AAG TTC Leu Ser Ala Asp Gly Thr Lys Phe Glu Gln His Asp Ser Tyr Lys Phe 435 440 445 450	1461
GTG GCG TTC AAC GCC GGG CCG AGG GTG TGC CTG GGC AAG GAC CTA GCC Val Ala Phe Asn Ala Gly Pro Arg Val Cys Leu Gly Lys Asp Leu Ala 455 460 465	1509
TAC CTG CAG ATG AAG AAC ATC GCC GGG AGC GTG CTG CTC CCG CAC CGC Tyr Leu Gln Met Lys Asn Ile Ala Gly Ser Val Leu Leu Arg His Arg 470 475 480	1557
CTG ACC GTG GCG CCG GGC CAC CGC GTG GAG CAG AAG ATG TCG CTC ACC Leu Thr Val Ala Pro Gly His Arg Val Glu Gln Lys Met Ser Leu Thr 485 490 495	1605
CTC TTC ATG AAG GGC GGG CTA CGG ATG GAG GTA CGT CCG CGC GAC CTC Leu Phe Met Lys Gly Gly Leu Arg Met Glu Val Arg Pro Arg Asp Leu 500 505 510	1653
GCC CCC GTC CTC GAC GAG CCC TGC GGC CTG GAC GCC GGC GCC GCC ACC Ala Pro Val Leu Asp Glu Pro Cys Gly Leu Asp Ala Gly Ala Ala Thr 515 520 525 530	1701
GCC GCC GCA GCA AGT GCC ACA GCG CCG TGC GCG TAGAAGACCT GGCACCGGCA Ala Ala Ala Ala Ser Ala Thr Ala Pro Cys Ala 535 540	1754
CGCGCCATGC ATGATTTCGTG CGTGCTAGCT GTTGAAGGGA CGCCGGACAT TGAATGTGTA	1814
GATAGGGCAG CAGTGCAAGA CCGTAAGTAA AATTGATGAT GGGTTTGGTG ACAACATTGA	1874
AGCCACTCCT TTCCAGAATT TACGACCCGG ATAGGAGAAA CAGGGAAACT TTGCAGATCA	1934
CAACACAAGA TCTAGCCAGC CGGGGATCTG ATCTGATTTG CGTCTGCTCG GAGCACGGGT	1994
GCATGGGAGA CCAAGGAGGA AAACAAAAA TAACAGAAAC AGAGTGAGCA ATATTTGTGA	2054
TTGTAGCCAC GGGAAAGAGA GAGGAGTAAT TAGTAATTC AATTGTGTTG CAGTAGCTCG	2114
GTGTTGGTGA CCAGATCATA GCCAACTAGG CTATTCTATT CTATTCTATT TTTGAAGATG	2174
ATTTTTC	2181

09713794 11500

## (2) INFORMATION FOR SEQ ID NO: 11:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATATATGGAT CCATGGAGGT GGGGACGTGG GCGGTGGTG

39

## (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

ATATATGGAT CCATGGAAGT TGGTACTTGG GCTGTTGTTG TTCTGCTGT TGCTGCTTAT

60

ATGGCTTGGT TTTGGAGAAT GTCTAGAGGT TTGAGAGGTC CAAGAGTTTG GCCAGTTTTC

120

GGTTCTTTGC CAGGCCTGCT GCAGCACGCC

150

## (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleotide

005TTT"46ZET260

(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "reverse"

**TATATAGAAT TCCTTCTACG CGCACGGCGC TGTGGCACTT GC**

42

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleotide

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..1623

ATG	GAA	GTT	GGT	ACT	TGG	GCT	GTT	GTT	GTT	TCT	GCT	GTT	GCT	GCT	TAT
Met	Glu	Val	Gly	Thr	Trp	Ala	Val	Val	Val	Ser	Ala	Val	Ala	Ala	Tyr
1				5					10					15	

48

ATG GCT TGG TTT TGG AGA ATG TCT AGA GGT TTG AGA GGT CCA AGA GTT  
Met Ala Trp Phe Trp Arg Met Ser Arg Gly Leu Arg Gly Pro Arg Val  
20 25 30

96

TGG CCA GTT TTG GGT TCT TTG CCA GGC CTG GTG CAG CAC GCC GAG GAC  
Trp Pro Val Leu Gly Ser Leu Pro Gly Leu Val Gln His Ala Glu Asp  
35 40 45

144

ATG CAC GAG TGG ATC GCC GGC AAC CTG CGC CGC GCG GGC GGC ACG TAC	192
Met His Glu Trp Ile Ala Gly Asn Leu Arg Arg Ala Gly Gly Thr Tyr	
50 55 60	
CAG ACC TGC ATC TTC GCC GTG CCC GGG GTG GCG CGC CGC GGC GGC CTG	240
Gln Thr Cys Ile Phe Ala Val Pro Gly Val Ala Arg Arg Gly Gly Leu	
65 70 75 80	
GTC ACC GTC ACC TGC GAC CCG CGC AAC CTG GAG CAC GTC CTG AAG GCG	288
Val Thr Val Thr Cys Asp Pro Arg Asn Leu Glu His Val Leu Lys Ala	
85 90 95	
CGC TTC GAC AAC TAC CCC AAG GGC CCC TTC TGG CAC GGC GTC TTC CGG	336
Arg Phe Asp Asn Tyr Pro Lys Gly Pro Phe Trp His Gly Val Phe Arg	
100 105 110	
GAC CTG CTC GGC GAC GGC ATC TTC AAT TCC GAC GGC GAC ACC TGG CTC	384
Asp Leu Leu Gly Asp Gly Ile Phe Asn Ser Asp Gly Asp Thr Trp Leu	
115 120 125	
GCG CAG CGC AAG ACG GCC GCG CTC GAG TTC ACC ACC CGC ACG CTC CGG	432
Ala Gln Arg Lys Thr Ala Ala Leu Glu Phe Thr Thr Arg Thr Leu Arg	
130 135 140	
ACG GCC ATG TCC CGC TGG GTC TCG CGC TCC ATC CAC GGC CGC CTC CTG	480
Thr Ala Met Ser Arg Trp Val Ser Arg Ser Ile His Gly Arg Leu Leu	
145 150 155 160	
CCC ATC CTG GCC GAC GCG GCC AAG GGC AAG GCG CAG GTG GAT CTC CAG	528
Pro Ile Leu Ala Asp Ala Ala Lys Gly Lys Ala Gln Val Asp Leu Gln	
165 170 175	
GAC CTC CTC CTC GCG CTC ACC TTC GAC AAC ATC TGC GGC CTG GCC TTC	576
Asp Leu Leu Leu Arg Leu Thr Phe Asp Asn Ile Cys Gly Leu Ala Phe	
180 185 190	
GGC AAG GAC CCG GAG ACG CTC GCC CAG GGC CTG CCG GAG AAC GAG TTC	624
Gly Lys Asp Pro Glu Thr Leu Ala Gln Gly Leu Pro Glu Asn Glu Phe	
195 200 205	
GCC TCC GCG TTC GAC CGC GCC ACC GAG GCC ACG CTC AAC CGC TTC ATC	672
Ala Ser Ala Phe Asp Arg Ala Thr Glu Ala Thr Leu Asn Arg Phe Ile	
210 215 220	
TTC CCG GAG TTC CTG TGG CGC TGC AAA AAG TGG CTG GGC CTC GGC ATG	720
Phe Pro Glu Phe Leu Trp Arg Cys Lys Lys Trp Leu Gly Leu Gly Met	
225 230 235 240	
GAG ACC ACG CTG ACC AGC AGC ATG GCC CAC GTC GAC CAG TAC CTC GCC	768
Glu Thr Thr Leu Thr Ser Ser Met Ala His Val Asp Gln Tyr Leu Ala	
245 250 255	
GCC GTC ATC AAG AAG CGC AAG CTC GAG CTC GCC GCC GGC AAC GGC AAA	816
Ala Val Ile Lys Lys Arg Lys Leu Glu Leu Ala Ala Gly Asn Gly Lys	
260 265 270	
TGC GAC ACG GCG GCG ACG CAC GAC GAC CTG CTC TCC CGG TTC ATG CGG	864
Cys Asp Thr Ala Ala Thr His Asp Asp Leu Leu Ser Arg Phe Met Arg	
275 280 285	
AAG GGT TCC TAC TCG GAC GAG TCG CTC CAG CAC GTG GCG CTC AAC TTC	912
Lys Gly Ser Tyr Ser Asp Glu Ser Leu Gln His Val Ala Leu Asn Phe	
290 295 300	
ATC CTC GCC GGC CGC GAC ACC TCC TCC GTG GCG CTC TCC TGG TTC TTC	960
Ile Leu Ala Gly Arg Asp Thr Ser Ser Val Ala Leu Ser Trp Phe Phe	
305 310 315 320	

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TGG	CTC	GTG	TCC	ACC	CAC	CCT	GCG	GTG	GAG	CGC	AAG	ATC	GTG	CGC	GAG	1008
Trp	Leu	Val	Ser	Thr	His	Pro	Ala	Val	Glu	Arg	Lys	Ile	Val	Arg	Glu	
				325					330					335		
CTC	TGC	TCC	GTT	CTC	GCC	GCG	TCA	CGG	GGC	GCC	CAT	GAC	CCG	GCA	TTG	1056
Leu	Cys	Ser	Val	Leu	Ala	Ala	Ser	Arg	Gly	Ala	His	Asp	Pro	Ala	Leu	
			340					345					350			
TGG	CTG	GCG	GAG	CCC	TTC	ACC	TTC	GAG	GAG	CTC	GAC	CGC	CTG	GTC	TAC	1104
Trp	Leu	Ala	Glu	Pro	Phe	Thr	Phe	Glu	Glu	Leu	Asp	Arg	Leu	Val	Tyr	
			355				360					365				
CTC	AAG	GCG	GCG	CTG	TCG	GAG	ACC	CTC	CGC	CTC	TAC	CCC	TCC	GTC	CCC	1152
Leu	Lys	Ala	Ala	Leu	Ser	Glu	Thr	Leu	Arg	Leu	Tyr	Pro	Ser	Val	Pro	
	370					375					380					
GAG	GAC	TCC	AAG	CAC	GTC	GTC	GCG	GAC	GAC	TAC	CTC	CCC	GAC	GGC	ACC	1200
Glu	Asp	Ser	Lys	His	Val	Val	Ala	Asp	Asp	Tyr	Leu	Pro	Asp	Gly	Thr	
	385				390					395				400		
TTC	GTG	CCG	GCC	GGG	TCG	TCG	GTC	ACC	TAC	TCC	ATA	TAC	TCG	GCG	GGG	1248
Phe	Val	Pro	Ala	Gly	Ser	Ser	Val	Thr	Tyr	Ser	Ile	Tyr	Ser	Ala	Gly	
				405					410					415		
CGC	ATG	AAG	GGG	GTG	TGG	GGG	GAG	GAC	TGC	CTC	GAG	TTC	CGG	CCG	GAG	1296
Arg	Met	Lys	Gly	Val	Trp	Gly	Glu	Asp	Cys	Leu	Glu	Phe	Arg	Pro	Glu	
			420				425						430			
CGA	TGG	CTG	TCG	GCC	GAC	GGC	ACC	AAG	TTC	GAG	CAG	CAC	GAC	TCG	TAC	1344
Arg	Trp	Leu	Ser	Ala	Asp	Gly	Thr	Lys	Phe	Glu	Gln	His	Asp	Ser	Tyr	
			435				440					445				
AAG	TTC	GTG	GCG	TTC	AAC	GCC	GGG	CCG	AGG	GTG	TGC	CTG	GGC	AAG	GAC	1392
Lys	Phe	Val	Ala	Phe	Asn	Ala	Gly	Pro	Arg	Val	Cys	Leu	Gly	Lys	Asp	
	450					455					460					
CTA	GCC	TAC	CTG	CAG	ATG	AAG	AAC	ATC	GCC	GGG	AGC	GTG	CTG	CTC	CGG	1440
Leu	Ala	Tyr	Leu	Gln	Met	Lys	Asn	Ile	Ala	Gly	Ser	Val	Leu	Leu	Arg	
	465				470					475					480	
CAC	CGC	CTG	ACC	GTG	GCG	CCG	GGC	CAC	CGC	GTG	GAG	CAG	AAG	ATG	TCG	1488
His	Arg	Leu	Thr	Val	Ala	Pro	Gly	His	Arg	Val	Glu	Gln	Lys	Met	Ser	
				485					490					495		
CTC	ACG	CTC	TTC	ATG	AAG	GGC	GGG	CTA	CGG	ATG	GAG	GTA	CGT	CCG	CGC	1536
Leu	Thr	Leu	Phe	Met	Lys	Gly	Gly	Leu	Arg	Met	Glu	Val	Arg	Pro	Arg	
			500					505					510			
GAC	CTC	GCC	CCC	GTC	CTC	GAC	GAG	CCC	TGC	GGC	CTG	GAC	GCC	GGC	GCC	1584
Asp	Leu	Ala	Pro	Val	Leu	Asp	Glu	Pro	Cys	Gly	Leu	Asp	Ala	Gly	Ala	
		515				520						525				
GCC	ACC	GCC	GCC	GCA	GCA	AGT	GCC	ACA	GCG	CCG	TGC	GCG	TAG			1626
Ala	Thr	Ala	Ala	Ala	Ala	Ser	Ala	Thr	Ala	Pro	Cys	Ala				
	530					535					540					

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